RAW SEQUENCE LISTING   DATE: 11/10/2003
PATENT APPLICATION: **US/09/424,686F**   TIME: 11:29:39

Input Set : **A:\pto.ln.txt**
Output Set: **N:\CRF4\11102003\I424686F.raw**

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 4 <110> APPLICANT: Hagen, Gustav
 5         Siegmund, Hans-Ulrich
 6         Weichel, Walter
 7         Wick, Maresa
 8         Zubov, Dmitry
10 <120> TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
rapeutic
11         Use
13 <130> FILE REFERENCE: Bayer 10,203
15 <140> CURRENT APPLICATION NUMBER: US 09/424,686F
17 <141> CURRENT FILING DATE: 1999-11-29
19 <150> PRIOR APPLICATION NUMBER: PCT/EP98/03468
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23 <160> NUMBER OF SEQ ID NOS: 32
25 <170> SOFTWARE: Microsoft Word
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 4042
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
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172 <211> LENGTH: 1132
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
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Input Set : **A:\pto.ln.txt**
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180     His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
181                 20              25              30
·183    Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
184             35              40              45
186     Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
187         50              55              60
189     Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
190     65              70              75              80
192     Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
193                 85              90              95
195     Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
196             100             105             110
198     Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
199             115             120             125
201     Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
202         130             135             140
204     Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
205     145             150             155             .160
207     Leu. Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
208             165             170             175
210     Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
211             180             185             190
213     Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
214         195             200             205
216     Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
217         210             215             220
219     Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
220     225             230             235             240
222     Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
223             245             250             255
225     Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
226             260             265             270
228     Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
229         275             280             285
231     Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
232         290             295             300
234     Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
235     305             310             315             320
237     Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
238             325             330             335
240     Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg·Pro
241             340             345             350
243     Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
244         355             360             365
246     Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
247     370             375             380
249     Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
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                    RAW SEQUENCE LISTING            DATE: 11/10/2003
                    PATENT APPLICATION:  US/09/424,686F    TIME: 11:29:39

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                        Output Set: N:\CRF4\11102003\I424686F.raw

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253                      405                410                 415
255    Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
256                      420                425                 430
258    Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
259                      435                440                 445
261    Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
262            450                455                460
264    Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
265    465                470                475                 480
267    Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
268                      485                490                 495
270    Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
271            500                505                510
273    Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
274            515                520                525
276    Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
277            530                535                540
279    Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
280    545                550                555                 560
282    Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
283                      565                570                 575
285    Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
286            580                585                590
288    Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
289            595                600                605
291    His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
292            610                615                620
294    Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
295    625                630                635                 640
297    Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
298                      645                650                655
300    Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
301            660                665                670
303    Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
304            675                680                685
306    Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
307            690                695                700
309    Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
310    705                710                715                 720
312    Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
313                      725                730                735
315    Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
316                      740                745                750
318    Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
319            755                760                765
321    Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
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Input Set : **A:\pto.ln.txt**
Output Set: **N:\CRF4\11102003\I424686F.raw**

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330     Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
331                 820             825             830
333     Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
334                 835             840             845
336     Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
337         850             855             860
339     Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
340     865             870             875             880
342     Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
343                 885             890             895
345     Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
346                 900             905             910
348     Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
349                 915             920             925
351     Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
352         930             935             940  ·
354     Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
355     945             950             955             960
357     Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
358                 965             970             975
360     Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
361                 980             985             990
363     Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
364                 995             1000            1005
366     Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
367         1010            1015            1020
369     Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
370     1025            1030            1035            1040
372     Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
373                 1045            1050            1055
375     Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
376                 1060            1065            1070
378     Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
379                 1075            1080            1085
381     Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
382         1090            1095            1100
384     Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
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388                 1125            1130
390 <210> SEQ ID NO: 3
391 <211> LENGTH: 1153
392 <212> TYPE: DNA
393 <213> ORGANISM: Homo sapiens ·
395 <400> SEQUENCE: 3
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/424,686F**

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Output Set: **N:\CRF4\11102003\I424686F.raw**